

Please amend the application as follows:

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IN THE CLAIMS:

GROUP 1600

Replace claims 22-27 with the following revised claims:

22. (Amended) A method for screening compounds for modulation of GABA_A receptor 1 transcription, comprising the steps of:

(a) transfecting a host cell with a suitable expression system comprising a nucleic acid molecule constituting a human GABA_A receptor 1 promoter P1a and/or a human GABA_A receptor 1 promoter P1b, or functionally equivalent modified forms thereof, or active fragments thereof, wherein the promoter or modified form thereof or active fragment thereof is coupled to a reporter gene;

(b) contacting a test compound with the cell; and

(c) determining whether the test compound modulates the level of expression of the reporter gene.

23. (Amended) The method according to claim 22, wherein the nucleic acid molecule of the expression system is selected from the group consisting of:

(a) a nucleic acid molecule comprising SEQ ID No: 1;

(b) a nucleic acid molecule comprising a nucleotide sequence capable of hybridizing, under stringent conditions to a nucleotide sequence complementary to SEQ ID NO: 1;

(c) a nucleic acid molecule comprising SEQ ID No: 2; and

(d) a nucleic acid molecule comprising a nucleotide sequence capable of hybridizing, under stringent conditions to a nucleotide sequence complementary to SEQ ID NO: 2.

24. (Amended) The method according to claim 22, wherein the reporter gene is selected from the group consisting of:

- (a) the firefly luciferase gene;
- (b) the bacterial chloramphenicol acetyl transferase (CAT) gene;
- (c) the β -galactosidase (β -Gal) gene; and
- (d) the green fluorescent protein (GFP) gene.

25. (Amended) The method according to claim 22, wherein the host cell endogenously expresses at least one GABA_B receptor 1.

26. (Amended) The method according to claim 22, wherein the host cell is further transfected with a suitable expression system comprising a nucleic acid molecule encoding at least one transcription factor.

27. (Amended) The method according to claim 26, wherein the transcription factor is selected from the group consisting of: CREB-1, CREB-2, CREM-1, ATF-1, ATF-2, ATF-3, ATF-4, Sp1, Sp2, Sp3, Sp4, AP-1 and AP-2.